

**FIGURE 1**

TTCGCCCTTCTGTGCTCTGCCTCTGAGGAGACCATGGGCCAGTATCTGAGTACCCTGCTGCTCCTGCTGGCCAC  
CCTAGCTGTGGCCCTGGCCTGGAGCCCCAAGGAGGAGGATAGGATAATCCCGGGTGGCATCTATAACGCAGACC  
TCAATGATGAGTGGGTACAGCGTGCCCTTCACTTCGCCATCAGCGAGTATAACAAGGCCACCAAAGATGACTAC  
TACAGACGTCCGCTGCGGGTACTAAGAGCCAGGCAACAGACCGTTGGGGGGGTGAATTACTTCTTCGACGTAGA  
GGTGGGCCGAACCATATGTACCAAGTCCCAGCCCAACTTGGACACCTGTGCCTTCCATGAACAGCCAGAACTGC  
AGAAGAAACAGTTGTGCTCTTTCGAGATCTACGAAGTTCCTGGGAGAACAGAAGGTCCCTGGTGAATTCCAGG  
TGTCAAGAAGCCTAGGGAAGGGCGA

**FIGURE 2**

GCCTCCGAGGAGACCATGGCCTGGCCCCTGTGCACCCTGCTGCTCCTGCTGGCCACCCAGGCTGTGGCCCTGGC  
CTGGAGCCCCCAGGAGGAGGACAGGATAATCGAGGGTGGCATCTATGATGCAGACCTCAATGATGAGCGGGTAC  
AGCGTGCCCTTCACTTTGTCATCAGCGAGTATAACAAGGCCACTGAAGATGAGTACTACAGACGCCTGCTGCGG  
GTGCTACGAGCCAGGGAGCAGATCGTGGGCGGGGTGAATTACTTCTTCGACATAGAGGTGGGCCGAACCATATG  
TACCAAGTCCCAGCCCAACTTGGACACCTGTGCCTTCCATGAACAGCCAGAACTGCAGAAGAAACAGTTGTGCT  
CTTTCCAGATCTACGAAGTTCCCTGGGAGGACAGAATGTCCCTGGTGAATTCCAGGTGTCAAGAAGCCTAGGGA  
TCTGTGCCAGGGAGTCACACTGACCACCTCCTACTCCCACCCCTTGTAGTGCTCCCACCCCTGGACTGGTGGCC  
CCCACCCCTGTGGGAGGTCTCCCCATGCACCTGCAGCAGGAGAAGACAGAGAAGGCTGCAGGAGGCCTTTGTTGC  
TCAGCAGGGGACTCTGCCCTCCCTCCTTCTTTGCTTCTCATAGCCCTGGTACATGGTACACACACCCCCACC  
TCCTGCAATTAAACAGTAGCATCACCTC

**FIGURE 3**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGCTTCCCTGGG  
 GCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTG  
 GTATTTCAAGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCTGGGAACATTGGGGAGGATGGAATCCTG  
 AGCTGCACTTTTGAACCTGACATCAAACCTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTT  
 GGTCCATGAGTTCAAAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTGAGAGCCGGACAGCAGTGT  
 TTGCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTAC  
 AAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCC  
 GGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCA  
 CAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAAC  
 TCTGAGAAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGAT  
 TGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAGTCACCTAC  
 AGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGC  
 CCTTACCTGATGCTAAAATAATGTGCCTTGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTAC  
 AGAACTATTTACCACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGG  
 AGTGAGCAAACAAGAGCAAGAAACAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATC  
 TTCAAAGACATATTAGAAGTTGGGAAAATAATTGATGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAAT  
 GCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGGGAGTGAGAGGACAGG  
 ATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCCTGGAAAG  
 TCTATCCCAACATATCCACATCTTATATTCCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGA  
 CTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAA  
 AGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAG  
 AGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 4**

MAQYLSTLLLLLATLAVALAWSPKEEDRIIPGGIYNADLNDEWVQRALHFAISEYNKATKDDYYRRPLRVLRAR  
QQTVGGVNYFFDVEVGRTICTKSQPNLDTCAFHEQPQLQKKQLCSFEIYVWPWENRRSLVNSRCQEA

Signal sequence.

amino acids 1-20

Tyrosine kinase phosphorylation site.

amino acids 57-64

N-myristoylation sites.

amino acids 32-37, 33-38

Myb DNA-binding domain repeat signature 1.

amino acids 21-29

Cystatin domain.

amino acids 32-137

## **FIGURE 5**

MAWPLCTLLLLLATQAVALLAWSPQEEDRIIEGGIYDADLNDERVQRALHFVISEYNKATEDEYYRLLRVLRAR  
EQIVGGVNYFFDIEVGRTICTKSQPNLDTCAFHEQPELQKKQLCSFQIYEVPWEDRMSLVNSRCQEA

Signal sequence.

amino acids 1-20

Tyrosine kinase phosphorylation sites.

amino acids 28-35, 57-64

N-myristoylation site.

amino acids 33-38

Myb DNA-binding domain repeat signature 1.

amino acids 21-29

Cystatin domain.

amino acids 32-137

## **FIGURE 6**

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKE  
GVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKCYIITSKGKGNANLEYKTG  
AFSMPEVNVDYNASSETLRCEAPRWFPQPTVWVASQVDQGANFSEVSNTSFELNSENVTMKVSVLYNVTINNT  
YSCMIENDIAKATGDIKVTSESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

Signal peptide.

amino acids 1-28

Transmembrane domain.

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220, 220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

Immunoglobulin domain.

amino acids 49-132